

Sequence Listing

(1) GENERAL INFORMATION

(i) APPLICANT: Meltzer and Trent

(ii) TITLE OF INVENTION: AIB1, A NOVEL RECEPTOR CO-ACTIVATOR
AMPLIFIED IN CANCER

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Klarquist Sparkman Campbell Leigh & Whinston, LLP

(B) STREET: One World Trade Center

121 S.W. Salmon Street, Suite 1600

(C) CITY: Portland

(D) STATE: Oregon

(E) COUNTRY: United States of America

(F) ZIP: 97204-2988

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Disk, 3-1/2 inch

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: Widows NT

(D) SOFTWARE: WordPerfect 7.0 & ASCII

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: William D. Noonan, M.D.

(B) REGISTRATION NUMBER: 30,878

(C) REFERENCE/DOCKET NUMBER: 4239-49944

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (503) 226-7391

(B) TELEFAX: (503) 228-9446

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6837 nucleotides; 1419 amino acid residues

(B) TYPE: Human DNA & Amino Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CG GCG GCG GCT GCG GCT TAG TCG GTG GCG GCC GGC GGC TGC GGG CTG AGC GGC
1 5 10 15
GAG TTT CCG ATT TAA AGC TGA GCT GCG AGG AAA ATG GCG GCG GGA GGA TCA AAA TAC
20 25 30 35

	TTG	CTG	GAT	GGT	GGA	CTC	AGA	GAC	CAA	TAA	AAA	TAA	ACT	GCT	TGA	ACA	TCC	TTT	GAC
	40						45					50					55		
	TGG	TTA	GCC	AGT	TGC	TGA	TGT	ATA	TTC	AAG	ATG	AGT	GGA	TTA	GGA	GAA	AAC	TTG	GAT
										Met	Ser	Gly	Leu	Gly	Glu	Asn	Leu	Asp	
5			60				65					70					75		
	CCA	CTG	GCC	AGT	GAT	TCA	CGA	AAA	CGC	AAA	TTG	CCA	TGT	GAT	ACT	CCA	GGA	CAA	GGT
	Pro	Leu	Ala	Ser	Asp	Ser	Arg	Lys	Arg	Lys	Leu	Pro	Cys	Asp	Thr	Pro	Gly	Gln	Gly
			80						85						90			95	
10	CTT	ACC	TGC	AGT	GGT	GAA	AAA	CGG	AGA	CGG	GAG	CAG	GAA	AGT	AAA	TAT	ATT	GAA	GAA
	Leu	Thr	Cys	Ser	Gly	Glu	Lys	Arg	Arg	Arg	Glu	Gln	Glu	Ser	Lys	Tyr	Ile	Glu	Glu
					100					105					110				
	TTG	GCT	GAG	CTG	ATA	TCT	GCC	AAT	CTT	AGT	GAT	ATT	GAC	AAT	TTC	AAT	GTC	AAA	CCA
	Leu	Ala	Glu	Leu	Ile	Ser	Ala	Asn	Leu	Ser	Asp	Ile	Asp	Asn	Phe	Asn	Val	Lys	Pro
	115				120					125					130				
15	GAT	AAA	TGT	GCG	ATT	TTA	AAG	GAA	ACA	GTA	AGA	CAG	ATA	CGT	CAA	ATA	AAA	GAG	CAA
	Asp	Lys	Cys	Ala	Ile	Leu	Lys	Glu	Thr	Val	Arg	Gln	Ile	Arg	Gln	Ile	Lys	Glu	Gln
	135				140					145					150				
	GGA	AAA	ACT	ATT	TCC	AAT	GAT	GAT	GAT	GTT	CAA	AAA	GCC	GAT	GTA	TCT	TCT	ACA	GGG
	Gly	Lys	Thr	Ile	Ser	Asn	Asp	Asp	Asp	Val	Gln	Lys	Ala	Asp	Val	Ser	Ser	Thr	Gly
			155					160					165					170	
20	CAG	GGA	GTT	ATT	GAT	AAA	GAC	TCC	TTA	GGA	CCG	CTT	TTA	CTT	CAG	GCA	TTG	GAT	GGT
	Gln	Gly	Val	Ile	Asp	Lys	Asp	Ser	Leu	Gly	Pro	Leu	Leu	Leu	Gln	Ala	Leu	Asp	Gly
			175					180					185					190	
25	TTT	CTA	TTT	GTG	GTG	AAT	CGA	GAC	GGA	AAC	ATT	GTA	TTT	GTA	TCA	GAA	AAT	GTC	ACA
	Phe	Leu	Phe	Val	Val	Asn	Arg	Asp	Gly	Asn	Ile	Val	Phe	Val	Ser	Glu	Asn	Val	Thr
				195				200							205				
	CAA	TAC	CTG	CAA	TAT	AAG	CAA	GAG	GAC	CTG	GTT	AAC	ACA	AGT	GTT	TAC	AAT	ATC	TTA
	Gln	Tyr	Leu	Gln	Tyr	Lys	Gln	Glu	Asp	Leu	Val	Asn	Thr	Ser	Val	Tyr	Asn	Ile	Leu
	210			215						220					225				
30	CAT	GAA	GAA	GAC	AGA	AAG	GAT	TTT	CTT	AAG	AAT	TTA	CCA	AAA	TCT	ACA	GTT	AAT	GGA
	His	Glu	Glu	Asp	Arg	Lys	Asp	Phe	Leu	Lys	Asn	Leu	Pro	Lys	Ser	Thr	Val	Asn	Gly
	230			235						240					245				
	GTT	TCC	TGG	ACA	AAT	GAG	ACC	CAA	AGA	CAA	AAA	AGC	CAT	ACA	TTT	AAT	TGC	CGT	ATG
	Val	Ser	Trp	Thr	Asn	Glu	Thr	Gln	Arg	Gln	Lys	Ser	His	Thr	Phe	Asn	Cys	Arg	Met
			250				255					260						265	
35	TTG	ATG	AAA	ACA	CCA	CAT	GAT	ATT	CTG	GAA	GAC	ATA	AAC	GCC	AGT	CCT	GAA	ATG	CGC
	Leu	Met	Lys	Thr	Pro	His	Asp	Ile	Leu	Glu	Asp	Ile	Asn	Ala	Ser	Pro	Glu	Met	Arg
			270					275						280				285	
40	CAG	AGA	TAT	GAA	ACA	ATG	CAG	TGC	TTT	GCC	CTG	TCT	CAG	CCA	CGA	GCT	ATG	ATG	GAG
	Gln	Arg	Tyr	Glu	Thr	Met	Gln	Cys	Phe	Ala	Leu	Ser	Gln	Pro	Arg	Ala	Met	Met	Glu
				290				295						300					
	GAA	GGG	GAA	GAT	TTG	CAA	TCT	TGT	ATG	ATC	TGT	GTG	GCA	CGC	CGC	ATT	ACT	ACA	GGA
	Glu	Gly	Glu	Asp	Leu	Gln	Ser	Cys	Met	Ile	Cys	Val	Ala	Arg	Arg	Ile	Thr	Thr	Gly
	305			310						315					320				
45	GAA	AGA	ACA	TTT	CCA	TCA	AAC	CCT	GAG	AGC	TTT	ATT	ACC	AGA	CAT	GAT	CTT	TCA	GGA
	Glu	Arg	Thr	Phe	Pro	Ser	Asn	Pro	Glu	Ser	Phe	Ile	Thr	Arg	His	Asp	Leu	Ser	Gly
	325			330						335					340				
	AAG	GTT	GTC	AAT	ATA	GAT	ACA	AAT	TCA	CTG	AGA	TCC	TCC	ATG	AGG	CCT	GGC	TTT	GAA
	Lys	Val	Val	Asn	Ile	Asp	Thr	Asn	Ser	Leu	Arg	Ser	Ser	Met	Arg	Pro	Gly	Phe	Glu
			345				350						355					360	
50	GAT	ATA	ATC	CGA	AGG	TGT	ATT	CAG	AGA	TTT	TTT	AGT	CTA	AAT	GAT	GGG	CAG	TCA	TGG
	Asp	Ile	Ile	Arg	Arg	Cys	Ile	Gln	Arg	Phe	Phe	Ser	Leu	Asn	Asp	Gly	Gln	Ser	Trp
				365				370						375				380	
55	TCC	CAG	AAA	CGT	CAC	TAT	CAA	GAA	GCT	TAT	CTT	AAT	GGC	CAT	GCA	GAA	ACC	CCA	GTA
	Ser	Gln	Lys	Arg	His	Tyr	Gln	Glu	Ala	Tyr	Leu	Asn	Gly	His	Ala	Glu	Thr	Pro	Val
				385				390						395					
	TAT	CGA	TTC	TCG	TTG	GCT	GAT	GGA	ACT	ATA	GTG	ACT	GCA	CAG	ACA	AAA	AGC	AAA	CTC
	Tyr	Arg	Phe	Ser	Leu	Ala	Asp	Gly	Thr	Ile	Val	Thr	Ala	Gln	Thr	Lys	Ser	Lys	Leu
	400				405					410					415				
60																			
	TTT	CGA	AAT	CCT	GTA	ACA	AAT	GAT	CGA	CAT	GGC	TTT	GTC	TCA	ACC	CAC	TTT	CTT	CAG
	Phe	Arg	Asn	Pro	Val	Thr	Asn	Asp	Arg	His	Gly	Phe	Val	Ser	Thr	His	Phe	Leu	Gln
	420				425						430						435		
65	AGA	GAA	CAG	AAT	GGA	TAT	AGA	CCA	AAC	CCA	AAT	CCT	GTT	GGA	CAA	GGG	ATT	AGA	CCA
	Arg	Glu	Gln	Asn	Gly	Tyr	Arg	Pro	Asn	Pro	Asn	Pro	Val	Gly	Gln	Gly	Ile	Arg	Pro
			440				445					450					455		
	CCT	ATG	GCT	GGA	TGC	AAC	AGT	TCG	GTA	GGC	GGC	ATG	AGT	ATG	TCG	CCA	AAC	CAA	GGC
	Pro	Met	Ala	Gly	Cys	Asn	Ser	Ser	Val	Gly	Gly	Met	Ser	Met	Ser	Pro	Asn	Gln	Gly
			460				465					470						475	
70	TTA	CAG	ATG	CCG	AGC	AGC	AGG	GCC	TAT	GGC	TTG	GCA	GAC	CCT	AGC	ACC	ACA	GGG	CAG
	Leu	Gln	Met	Pro	Ser	Ser	Arg	Ala	Tyr	Gly	Leu	Ala	Asp	Pro	Ser	Thr	Thr	Gly	Gln

[illegible]

GGC TCA AGT CCT CCA GTA AAA AAT ATC AGT GCT TTC CCC ATG TTA CCA AAG CAA CCC
Gly Ser Ser Pro Pro Val Lys Asn Ile Ser Ala Phe Pro Met Leu Pro Lys Gln Pro
935 940 945 950

5 ATG TTG GGT GGG AAT CCA AGA ATG ATG GAT AGT CAG GAA AAT TAT GGC TCA AGT ATG
Met Leu Gly Gly Asn Pro Arg Met Met Asp Ser Gln Glu Asn Tyr Gly Ser Ser Met
955 960 965

GGT GGG CCA AAC CGA AAT GTG ACT GTG ACT CAG ACT CCT TCC TCA GGA GAC TGG GGC
Gly Gly Pro Asn Arg Asn Val Thr Val Thr Gln Thr Pro Ser Ser Gly Asp Trp Gly
970 975 980 985

10 TTA CCA AAC TCA AAG GCC GGC AGA ATG GAA CCT ATG AAT TCA AAC TCC ATG GGA AGA
Leu Pro Asn Ser Lys Ala Gly Arg Met Glu Pro Met Asn Ser Asn Ser Met Gly Arg
990 995 1000 1005

CCA GGA GGA GAT TAT AAT ACT TCT TTA CCC AGA CCT GCA CTG GGT GGC TCT ATT CCC
Pro Gly Gly Asp Tyr Asn Thr Ser Leu Pro Arg Pro Ala Leu Gly Gly Ser Ile Pro
1010 1015 1020 1025

15 ACA TTG CCT CTT CGG TCT AAT AGC ATA CCA GGT GCG AGA CCA GTA TTG CAA CAG CAG
Thr Leu Pro Leu Arg Ser Asn Ser Ile Pro Gly Ala Arg Pro Val Leu Gln Gln Gln
1030 1035 1040 1045

20 CAG CAG ATG CTT CAA ATG AGG CCT GGT GAA ATC CCC ATG GGA ATG GGC GCT AAT CCC
Gln Gln Met Leu Gln Met Arg Pro Gly Ile Pro Met Gly Met Gly Ala Asn Pro
1050 1055 1060

TAT GGC CAA GCA GCA GCA TCT AAC CAA CTG GGT TCC TGG CCC GAT GGC ATG TTG TCC
Tyr Gly Gln Ala Ala Ala Ser Asn Gln Leu Gly Ser Trp Pro Asp Gly Met Leu Ser
1065 1070 1075 1080

25 ATG GAA CAA GTT TCT CAT GGC ACT CAA AAT AGG CCT CTT CTT AGG AAT TCC CTG GAT
Met Glu Gln Val Ser His Gly Thr Gln Asn Arg Pro Leu Leu Arg Asn Ser Leu Asp
1085 1090 1095 1100

GAT CTT GTT GGG CCA CCT TCC AAC CTG GAA GGC CAG AGT GAC GAA AGA GCA TTA TTG
Asp Leu Val Gly Pro Pro Ser Asn Leu Glu Gly Gln Ser Asp Glu Arg Ala Leu Leu
1105 1110 1115 1120

30 GAC CAG CTG CAC ACT CTT CTC AGC AAC ACA GAT GCC ACA GGC CTG GAA GAA ATT GAC
Asp Gln Leu His Thr Leu Leu Ser Asn Thr Asp Ala Thr Gly Leu Glu Glu Ile Asp
1125 1130 1135 1140

35 AGA GCT TTG GGC ATT CCT GAA CTT GTC AAT CAG GGA CAG GCA TTA GAG CCC AAA CAG
Arg Ala Leu Gly Ile Pro Glu Leu Val Asn Gln Gly Gln Ala Leu Glu Pro Lys Gln
1145 1150 1155

GAT GCT TTC CAA GGC CAA GAA GCA GCA GTA ATG ATG GAT CAG AAG GCA GGA TTA TAT
Asp Ala Phe Gln Gly Gln Glu Ala Ala Val Met Met Asp Gln Lys Ala Gly Leu Tyr
1160 1165 1170 1175

40 GGA CAG ACA TAC CCA GCA CAG GGG CCT CCA ATG CAA GGA GGC TTT CAT CTT CAG GGA
Gly Gln Thr Tyr Pro Ala Gln Gly Pro Pro Met Gln Gly Gly Phe His Leu Gln Gly
1180 1185 1190 1195

CAA TCA CCA TCT TTT AAC TCT ATG ATG AAT CAG ATG AAC CAG CAA GGC AAT TTT CCT
Gln Ser Pro Ser Phe Asn Ser Met Met Asn Gln Met Asn Gln Gln Gly Asn Phe Pro
1200 1205 1210 1215

45 CTC CAA GGA ATG CAC CCA CGA GCC AAC ATC ATG AGA CCC CGG ACA AAC ACC CCC AAG
Leu Gln Gly Met His Pro Arg Ala Asn Ile Met Arg Pro Arg Thr Asn Thr Pro Lys
1220 1225 1230 1235

50 CAA CTT AGA ATG CAG CTT CAG CAG AGG CTG CAG GGC CAG CAG TTT TTG AAT CAG AGC
Gln Leu Arg Met Gln Leu Gln Gln Arg Leu Gln Gly Gln Gln Phe Leu Asn Gln Ser
1240 1245 1250

CGA CAG GCA CTT GAA TTG AAA ATG GAA AAC CCT ACT GCT GGT GGT GCT GCG GTG ATG
Arg Gln Ala Leu Glu Leu Lys Met Glu Asn Pro Thr Ala Gly Gly Ala Val Met
1255 1260 1265 1270

55 AGG CCT ATG ATG CAG CCC CAG CAG GGT TTT CTT AAT GCT CAA ATG GTC GCC CAA CGC
Arg Pro Met Met Gln Pro Gln Gln Gly Phe Leu Asn Ala Gln Met Val Ala Gln Arg
1275 1280 1285 1290

60 AGC AGA GAG CTG CTA AGT CAT CAC TTC CGA CAA CAG AGG GTG GCT ATG ATG ATG CAG
Ser Arg Glu Leu Leu Ser His His Phe Arg Gln Gln Arg Val Ala Met Met Met Gln
1295 1300 1305 1310

CAG CAG CAG CAG CAG CAA CAG CAG CAG CAG CAG CAG CAG CAG CAA CAG CAA CAG
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
1315 1320 1325 1330

65 CAA CAG CAA CAG CAG CAA CAG CAG CAA ACC CAG GCC TTC AGC CCA CCT CCT AAT GTG
Gln Gln Gln Gln Gln Gln Gln Gln Gln Thr Gln Ala Phe Ser Pro Pro Pro Asn Val
1335 1340 1345

ACT GCT TCC CCC AGC ATG GAT GGG CTT TTG GCA GGA CCC ACA ATG CCA CAA GCT CCT
Thr Ala Ser Pro Ser Met Asp Gly Leu Leu Ala Gly Pro Thr Met Pro Gln Ala Pro
1350 1355 1360 1365

70 CCG CAA CAG TTT CCA TAT CAA CCA AAT TAT GGA ATG GGA CAA CAA CCA GAT CCA GCC

	Pro	Gln	Gln	Phe	Pro	Tyr	Gln	Pro	Asn	Tyr	Gly	Met	Gly	Gln	Gln	Pro	Asp	Pro	Ala
	1370						1375					1380					1385		
	TTT	GGT	CGA	GTG	TCT	AGT	CCT	CCC	AAT	GCA	ATG	ATG	TCG	TCA	AGA	ATG	GGT	CCC	TCC
5	Phe	Gly	Arg	Val	Ser	Ser	Pro	Pro	Asn	Ala	Met	Met	Ser	Ser	Arg	Met	Gly	Pro	Ser
	1390						1395						1400				1405		
	CAG	AAT	CCC	ATG	ATG	CAA	CAC	CCG	CAG	GCT	GCA	TCC	ATC	TAT	CAG	TCC	TCA	GAA	ATG
	Gln	Asn	Pro	Met	Met	Gln	His	Pro	Gln	Ala	Ala	Ser	Ile	Tyr	Gln	Ser	Ser	Glu	Met
	1410						1415						1420				1425		
10	AAG	GGC	TGG	CCA	TCA	GGA	AAT	TTG	GCC	AGG	AAC	AGC	TCC	TTT	TCC	CAG	CAG	CAG	TTT
	Lys	Gly	Trp	Pro	Ser	Gly	Asn	Leu	Ala	Arg	Asn	Ser	Ser	Phe	Ser	Gln	Gln	Gln	Phe
	1430						1435						1440						
	GCC	CAC	CAG	GGG	AAT	CCT	GCA	GTG	TAT	AGT	ATG	GTG	CAC	ATG	AAT	GGC	AGC	AGT	GGT
	Ala	His	Gln	Gly	Asn	Pro	Ala	Val	Tyr	Ser	Met	Val	His	Met	Asn	Gly	Ser	Ser	Gly
	1445					1450				1455			1460						
15	CAC	ATG	GGA	CAG	ATG	AAC	ATG	AAC	CCC	ATG	CCC	ATG	TCT	GGC	ATG	CCT	ATG	GGT	CCT
	His	Met	Gly	Gln	Met	Asn	Met	Asn	Pro	Met	Pro	Met	Ser	Gly	Met	Pro	Met	Gly	Pro
	1465					1470				1475			1480						
	GAT	CAG	AAA	TAC	TGC	TGA	CAT	CTC	TGC	ACC	AGG	ACC	TCT	TAA	GGA	AAC	CAC	TGT	ACA
	Asp	Gln	Lys	Tyr	Cys	***													
20	1485					1490				1495			1500						
	AAT	GAC	ACT	GCA	CTA	GGA	TTA	TTG	GGA	AGG	AAT	CAT	TGT	TCC	AGG	CAT	CCA	TCT	TGG
	1505					1510				1515			1520						
	AAG	AAA	GGA	CCA	GCT	TTG	AGC	TCC	ATC	AAG	GGT	ATT	TTA	AGT	GAT	GTC	ATT	TGA	GCA
	1525					1530				1535			1540						
25	GGA	CTG	GAT	TTT	AAG	CCG	AAG	GGC	AAT	ATC	TAC	GTG	TTT	TTC	CCC	CCT	CCT	TCT	GCT
	1540				1545					1550			1555						
	GTG	TAT	CAT	GGT	GTT	CAA	AAC	AGA	AAT	GTT	TTT	TGG	CAT	TCC	ACC	TCC	TAG	GGA	TAT
	1560				1565					1570			1575						
30	AAT	TCT	GGA	GAC	ATG	GAG	TGT	TAC	TGA	TCA	TAA	AAC	TTT	TGT	GTC	ACT	TTT	TTC	TGC
	1580				1585					1590			1595						
	CTT	GCT	AGC	CAA	AAT	CTC	TTA	AAT	ACA	CGT	AGG	TGG	GCC	AGA	GAA	CAT	TGG	AAG	AAT
	1600				1605					1610			1615						
	CAA	GAG	AGA	TTA	GAA	TAT	CTG	GTT	TCT	CTA	GTT	GCA	GTA	TTG	GAC	AAA	GAG	CAT	AGT
	1620				1625					1630			1635						
35	CCC	AGC	CTT	CAG	GTG	TAG	TAG	TTC	TGT	GTT	GAC	CCT	TTG	TCC	AGT	GGA	ATT	GGT	GAT
	1635				1640					1645			1650						
	TCT	GAA	TTG	TCC	TTT	ACT	AAT	GGT	GTT	GAG	TTG	CTC	TGT	CCC	TAT	TAT	TTG	CCC	TAG
	1655				1660					1665			1670						
40	GCT	TTC	TCC	TAA	TGA	AGG	TTT	TCA	TTT	GCC	ATT	CAT	GTC	CTG	TAA	TAC	TTC	ACC	TCC
	1675				1680					1685			1690						
	AGG	AAC	TGT	CAT	GGA	TGT	CCA	AAT	GGC	TTT	GCA	GAA	AGG	AAA	TGA	GAT	GAC	AGT	ATT
	1695				1700					1705			1710						
45	TAA	TCG	CAG	CAG	TAG	CAA	ACT	TTT	CAC	ATG	CTA	ATG	TGC	AGC	TGA	GTG	CAC	TTT	ATT
	1715				1720					1725			1730						
	TAA	AAA	GAA	TGG	ATA	AAT	GCA	ATA	TTC	TTG	AGG	TCT	TGA	GGG	AAT	AGT	GAA	ACA	CAT
	1730				1735					1740			1745						
	TCC	TGG	TTT	TTG	CCT	ACA	CTT	ACG	TGT	TAG	ACA	AGT	ACT	ATG	ATT	TTT	TTT	TTA	AAG
	1750				1755					1760			1765						
50	TAC	TGG	TGT	CAC	CCT	TTG	CCT	ATA	TGG	TAG	AGC	AAT	AAT	GCT	TTT	TAA	AAA	TAA	ACT
	1770				1775					1780			1785						
	TCT	GAA	AAC	CCA	AGG	CCA	GGT	ACT	GCA	TTC	TGA	ATC	AGA	ATC	TCG	CAG	TGT	TTC	TGT
	1790				1795					1800			1805						
55	GAA	TAG	ATT	TTT	TTG	TAA	ATA	TGA	CCT	TTA	AGA	TAT	TGT	ATT	ATG	TAA	AAT	ATG	TAT
	1810				1815					1820			1825						
	ATA	CCT	TTT	TTT	GTA	GGT	CAC	AAC	AAC	TCA	TTT	TTA	CAG	AGT	TTG	TGA	AGC	TAA	ATA
	1825				1830					1835			1840						
	TTT	AAC	ATT	GTT	GAT	TTC	AGT	AAG	CTG	TGT	GGT	GAG	GCT	ACC	AGT	GGA	AGA	GAC	ATC
	1845				1850					1855			1860						
60	CCT	TGA	CTT	TTG	TGG	CCT	GGG	GGA	GGG	GTA	GTG	CTC	CAC	AGC	TTT	TCC	TTC	CCC	ACC
	1865				1870					1875			1880						
	CCC	CAG	CCT	TAG	ATG	CCT	CGC	TCT	TTT	CAA	TCT	CTT	AAT	CTA	AAT	GCT	TTT	TAA	AGA
	1885				1890					1895			1900						
	GAT	TAT	TTG	TTT	AGA	TGT	AGG	CAT	TTT	AAT	TTT	TTA	AAA	ATT	CCT	CTA	CCA	GAA	CTA
65	1905				1910					1915			1920						
	AGC	ACT	TTG	TTA	ATT	TGG	GGG	GAA	AGA	ATA	GAT	ATG	GGG	AAA	TAA	ACT	TAA	AAA	AAA
	1925				1930					1935			1940						
	ATC	AGG	AAT	TTA	AAA	AAA	CGA	GCA	ATT	TGA	AGA	GAA	TCT	TTT	GGA	TTT	TAA	GCA	GTG
	1945				1950					1955			1960						
70	CGA	AAT	AAT	AGC	AAT	TCA	TGG	GCT	GTG	TGT	GTG	GTA	TGT	GTG	TGT	GTG	TGT	GTG	GTG
	1960				1965					1970			1975						

TAT GTT TAA TTA TGT TAC CTT TTC ATC CCC TTT AGG AGC GTT TTC AGA TTT TGG TTG
 1980 1985 1990 1995
 CTA AGA CCT GAA TCC CAT ATT GAG ATC TCG AGT AGA ATC CTT GGT GTG GTT TCT GGT
 2000 2005 2010
 5 GTC TGC TCA GCT GTC CCC TCA TTC TAC TAA TGT GAT GCT TTC ATT ATG TCC CTG TGG
 2015 2020 2025 2030
 ATT AGA ATA GTG TCA GTT ATT TCT TAA GTA ACT CAG TAC CCA GAA CAG CCA GTT TTA
 2035 2040 2045 2050
 10 CTG TGA TTC AGA GCC ACA GTC TAA CTG AGC ACC TTT TAA ACC CCT CCC TCT TCT GCC
 2055 2060 2065 2070
 CCC TAC CAC TTT TCT GCT GTT GCC TCT CTT TGA CAC CTG TTT TAG TCA GTT GGG AGG
 2075 2080 2085 2090
 AAG GGA AAA ATC AAG TTT AAT TCC CTT TAT CTG GGT TAA TTC ATT TGG TTC AAA TAG
 2095 2100 2105
 15 TTG ACG GAA TTG GGT TTC TGA ATG TCT GTG AAT TTC AGA GGT CTC TGC TAG CCT TGG
 2110 2115 2120 2125
 TAT CAT TTT CTA GCA ATA ACT GAG AGC CAG TTA ATT TTA AGA ATT TCA CAC ATT TAG
 2130 2135 2140 2145
 20 CCA ATC TTT CTA GAT GTC TCT GAA GGT AAG ATC ATT TAA TAT CTT TGA TAT GCT TAC
 2150 2155 2160 2165
 GAG TAA GTG AAT CCT GAT TAT TTC CAG ACC CAC CAC CAG AGT GGA TCT TAT TTT CAA
 2170 2175 2180 2185
 AGC AGT ATA GAC AAT TAT GAG TTT GCC CTC TTT CCC CTA CCA AGT TCA AAA TAT ATC
 2190 2195 2200
 25 TAA GAA AGA TTG TAA ATC CGA AAA CTT CCA TTG TAG TGG CCT GTG CTT TTC AGA TAG
 2205 2210 2215 2220
 TAT ACT CTC CTG TTT GGA GAC AGA GGA AGA ACC AGG TCA GTC TGT CTC TTT TTC AGC
 2225 2230 2235 2240
 30 TCA ATT GTA TCT GAC CCT TCT TTA AGT TAT GTG TGT GGG GAG AAA TAG AAT GGT GCT
 2245 2250 2255 2260
 CTT ATC TTT CTT GAC TTT AAA AAA ATT ATT AAA AAC AAA AAA AAA AAA AA
 2265 2270 2275

(2) INFORMATION FOR SEQ ID NO: 2:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186

(B) TYPE: amino acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Leu Gln Ala Leu Asp Gly Phe Leu Phe Val Val Asn Arg Asp Gly Asn Ile Val
 1 5 10 15
 Phe Val Ser Glu Asn Val Thr Gln Tyr Leu Gln Tyr Lys Gln Glu Asp Leu Val Asn
 20 25 30 35
 Thr Ser Val Tyr Asn Ile Leu His Glu Glu Asp Arg Lys Asp Phe Leu Lys Asn Leu
 40 45 50 55
 Pro Lys Ser Thr Val Asn Gly Val Ser Trp Thr Asn Glu Thr Gln Arg Gln Lys Ser
 60 65 70 75
 50 His Thr Phe Asn Cys Arg Met Leu Met Lys Thr Pro His Asp Ile Leu Glu Asp Ile
 80 85 90 95
 Asn Ala Ser Pro Glu Met Arg Gln Arg Tyr Glu Thr Met Gln Cys Phe Ala Leu Ser
 100 105 110 115
 Gln Pro Arg Ala Met Met Glu Glu Gly Glu Asp Leu Gln Ser Cys Met Ile Cys Val
 120 125 130 135
 Ala Arg Arg Ile Thr Thr Gly Glu Arg Thr Phe Pro Ser Asn Pro Glu Ser Phe Ile
 140 145 150 155
 Thr Arg His Asp Leu Ser Gly Lys Val Val Asn Ile Asp Thr Asn Ser Leu Arg Ser
 160 165 170 175
 60 Ser Met Arg Pro Gly Phe Glu Asp Ile Ile Arg Arg Cys Ile Gln
 175 180 185

(2) INFORMATION FOR SEQ ID NO: 3:

65 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73

(B) TYPE: amino acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

5 Arg Lys Arg Lys Leu Pro Cys Asp Thr Pro Gly Gln Gly Leu Thr Cys Ser Gly Glu
1 5 10 15
Lys Arg Arg Arg Glu Gln Glu Ser Lys Tyr Ile Glu Glu Leu Ala Glu Leu Ile Ser
20 25 130 135
Ala Asn Leu Ser Asp Ile Asp Asn Phe Asn Val Lys Pro Asp Lys Cys Ala Ile Leu
140 145 150 155
10 Lys Glu Thr Val Arg Gln Ile Arg Gln Ile Lys Glu Gln Gly Lys Thr
160 165 170

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 1419
(B) TYPE: human amino acid of AIB1
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ser Gly Leu Gly Glu Asn Leu Asp Pro Leu Ala Ser Asp Ser Arg Lys Arg Lys
1 5 10 15
Leu Pro Cys Asp Thr Pro Gly Gln Gly Leu Thr Cys Ser Gly Glu Lys Arg Arg Arg
20 25 30 35
25 Glu Gln Glu Ser Lys Tyr Ile Glu Glu Leu Ala Glu Leu Ile Ser Ala Asn Leu Ser
40 45 50 55
Asp Ile Asp Asn Phe Asn Val Lys Pro Asp Lys Cys Ala Ile Leu Lys Glu Thr Val
60 65 70 75
30 Arg Gln Ile Arg Gln Ile Lys Glu Gln Gly Lys Thr Ile Ser Asn Asp Asp Asp Val
80 85 90 95
Gln Lys Ala Asp Val Ser Ser Thr Gly Gln Gly Val Ile Asp Lys Asp Ser Leu Gly
100 105 110
Pro Leu Leu Leu Gln Ala Leu Asp Gly Phe Leu Phe Val Val Asn Arg Asp Gly Asn
115 120 125 130
35 Ile Val Phe Val Ser Glu Asn Val Thr Gln Tyr Leu Gln Tyr Lys Gln Glu Asp Leu
135 140 145 150
Val Asn Thr Ser Val Tyr Asn Ile Leu His Glu Glu Asp Arg Lys Asp Phe Leu Lys
155 160 165 170
40 Asn Leu Pro Lys Ser Thr Val Asn Gly Val Ser Trp Thr Asn Glu Thr Gln Arg Gln
175 180 185 190
Lys Ser His Thr Phe Asn Cys Arg Met Leu Met Lys Thr Pro His Asp Ile Leu Glu
195 200 205
Asp Ile Asn Ala Ser Pro Glu Met Arg Gln Arg Tyr Glu Thr Met Gln Cys Phe Ala
210 215 220 225
45 Leu Ser Gln Pro Arg Ala Met Met Glu Glu Gly Glu Asp Leu Gln Ser Cys Met Ile
230 235 240 245
Cys Val Ala Arg Arg Ile Thr Thr Gly Glu Arg Thr Phe Pro Ser Asn Pro Glu Ser
250 255 260 265
50 Phe Ile Thr Arg His Asp Leu Ser Gly Lys Val Val Asn Ile Asp Thr Asn Ser Leu
270 275 280 285
Arg Ser Ser Met Arg Pro Gly Phe Glu Asp Ile Ile Arg Arg Cys Ile Gln Arg Phe
290 295 300
Phe Ser Leu Asn Asp Gly Gln Ser Trp Ser Gln Lys Arg His Tyr Gln Glu Ala Tyr
305 310 315 320
55 Leu Asn Gly His Ala Glu Thr Pro Val Tyr Arg Phe Ser Leu Ala Asp Gly Thr Ile
325 330 335 340
Val Thr Ala Gln Thr Lys Ser Lys Leu Phe Arg Asn Pro Val Thr Asn Asp Arg His
345 350 355 360
60 Gly Phe Val Ser Thr His Phe Leu Gln Arg Glu Gln Asn Gly Tyr Arg Pro Asn Pro
365 370 375 380
Asn Pro Val Gly Gln Gly Ile Arg Pro Pro Met Ala Gly Cys Asn Ser Ser Val Gly
385 390 395
Gly Met Ser Met Ser Pro Asn Gln Gly Leu Gln Met Pro Ser Ser Arg Ala Tyr Gly
400 405 410 415
65 Leu Ala Asp Pro Ser Thr Thr Gly Gln Met Ser Gly Ala Arg Tyr Gly Ser Ser
420 425 430 435
Asn Ile Ala Ser Leu Thr Pro Gly Pro Gly Met Gln Ser Pro Ser Ser Tyr Gln Asn
440 445 450 455

	Asn	Asn	Tyr	Gly	Leu	Asn	Met	Ser	Ser	Pro	Pro	His	Gly	Ser	Pro	Gly	Leu	Ala	Pro	
				460						465				470					475	
	Asn	Gln	Gln	Asn	Ile	Met	Ile	Ser	Pro	Arg	Asn	Arg	Gly	Ser	Pro	Lys	Ile	Ala	Ser	
				480						485					490					
5	His	Gln	Phe	Ser	Pro	Val	Ala	Gly	Val	His	Ser	Pro	Met	Ala	Ser	Ser	Gly	Asn	Thr	
	495				500					505					510					
	Gly	Asn	His	Ser	Phe	Ser	Ser	Ser	Leu	Ser	Ala	Leu	Gln	Ala	Ile	Ser	Glu	Gly		
	515				520					525					530					
10	Val	Gly	Thr	Ser	Leu	Leu	Ser	Thr	Leu	Ser	Ser	Pro	Gly	Pro	Lys	Leu	Asp	Asn	Ser	
	535				540					545					550					
	Pro	Asn	Met	Asn	Ile	Thr	Gln	Pro	Ser	Lys	Val	Ser	Asn	Gln	Asp	Ser	Lys	Ser	Pro	
				555					560					565					570	
	Leu	Gly	Phe	Tyr	Cys	Asp	Gln	Asn	Pro	Val	Glu	Ser	Ser	Met	Cys	Gln	Ser	Asn	Ser	
				575					580					585						
15	Arg	Asp	His	Leu	Ser	Asp	Lys	Glu	Ser	Lys	Glu	Ser	Ser	Val	Glu	Gly	Ala	Glu	Asn	
	590				595					600					605					
	Gln	Arg	Gly	Pro	Leu	Glu	Ser	Lys	Gly	His	Lys	Lys	Leu	Leu	Gln	Leu	Thr	Cys		
	610				615					620					625					
20	Ser	Ser	Asp	Asp	Arg	Gly	His	Ser	Ser	Leu	Thr	Asn	Ser	Pro	Leu	Asp	Ser	Ser	Cys	
	630				635					640					645					
	Lys	Glu	Ser	Ser	Val	Ser	Val	Thr	Ser	Pro	Ser	Gly	Val	Ser	Ser	Ser	Thr	Ser	Gly	
				650					655					660					665	
	Gly	Val	Ser	Ser	Thr	Ser	Asn	Met	His	Gly	Ser	Leu	Leu	Gln	Glu	Lys	His	Arg	Ile	
				670					675					680						
25	Leu	His	Lys	Leu	Leu	Gln	Asn	Gly	Asn	Ser	Pro	Ala	Glu	Val	Ala	Lys	Ile	Thr	Ala	
	685				690					695					700					
	Glu	Ala	Thr	Gly	Lys	Asp	Thr	Ser	Ser	Ile	Thr	Ser	Cys	Gly	Asp	Gly	Asn	Val	Val	
	705				710					715					720					
30	Lys	Gln	Glu	Gln	Leu	Ser	Pro	Lys	Lys	Lys	Glu	Asn	Asn	Ala	Leu	Leu	Arg	Tyr	Leu	
	725				730					735					740					
	Leu	Asp	Arg	Asp	Asp	Pro	Ser	Asp	Ala	Leu	Ser	Lys	Glu	Leu	Gln	Pro	Gln	Val	Glu	
				745					750					755					760	
	Gly	Val	Asp	Asn	Lys	Met	Ser	Gln	Cys	Thr	Ser	Ser	Thr	Ile	Pro	Ser	Ser	Ser	Gln	
				765					770					775						
35	Glu	Lys	Asp	Pro	Lys	Ile	Lys	Thr	Glu	Thr	Ser	Glu	Glu	Gly	Ser	Gly	Asp	Leu	Asp	
	780				785					790					795					
	Asn	Leu	Asp	Ala	Ile	Leu	Gly	Asp	Leu	Thr	Ser	Ser	Asp	Phe	Tyr	Asn	Asn	Ser	Ile	
	800				805					810					815					
40	Ser	Ser	Asn	Gly	Ser	His	Leu	Gly	Thr	Lys	Gln	Gln	Val	Phe	Gln	Gly	Thr	Asn	Ser	
				820					825					830					835	
	Leu	Gly	Leu	Lys	Ser	Ser	Gln	Ser	Val	Gln	Ser	Ile	Arg	Pro	Pro	Tyr	Asn	Arg	Ala	
				840					845					850					855	
	Val	Ser	Leu	Asp	Ser	Pro	Val	Ser	Val	Gly	Ser	Ser	Pro	Pro	Val	Lys	Asn	Ile	Ser	
				860					865					870						
45	Ala	Phe	Pro	Met	Leu	Pro	Lys	Gln	Pro	Met	Leu	Gly	Gly	Asn	Pro	Arg	Met	Met	Asp	
	875				880					885				890						
	Ser	Gln	Glu	Asn	Tyr	Gly	Ser	Ser	Met	Gly	Gly	Pro	Asn	Arg	Asn	Val	Thr	Val	Thr	
	895				900					905				910						
50	Gln	Thr	Pro	Ser	Ser	Gly	Asp	Trp	Gly	Leu	Pro	Asn	Ser	Lys	Ala	Gly	Arg	Met	Glu	
				915					920					925					930	
	Pro	Met	Asn	Ser	Asn	Ser	Met	Gly	Arg	Pro	Gly	Gly	Asp	Tyr	Asn	Thr	Ser	Leu	Pro	
				935					940					945					950	
	Arg	Pro	Ala	Leu	Gly	Gly	Ser	Ile	Pro	Thr	Leu	Pro	Leu	Arg	Ser	Asn	Ser	Ile	Pro	
				955					960					965						
55	Gly	Ala	Arg	Pro	Val	Leu	Gln	Gln	Gln	Gln	Gln	Met	Leu	Gln	Met	Arg	Pro	Gly	Glu	
	970				975					980				985						
	Ile	Pro	Met	Gly	Met	Gly	Ala	Asn	Pro	Tyr	Gly	Gln	Ala	Ala	Ala	Ser	Asn	Gln	Leu	
	990				995					1000				1005						
60	Gly	Ser	Trp	Pro	Asp	Gly	Met	Leu	Ser	Met	Glu	Gln	Val	Ser	His	Gly	Thr	Gln	Asn	
				1010					1015					1020					1025	
	Arg	Pro	Leu	Leu	Arg	Asn	Ser	Leu	Asp	Asp	Leu	Val	Gly	Pro	Pro	Ser	Asn	Leu	Glu	
				1030					1035					1040						
	1045																			
65	Gly	Gln	Ser	Asp	Glu	Arg	Ala	Leu	Leu	Asp	Gln	Leu	His	Thr	Leu	Leu	Ser	Asn	Thr	
				1050					1055					1060						
	Asp	Ala	Thr	Gly	Leu	Glu	Glu	Ile	Asp	Arg	Ala	Leu	Gly	Ile	Pro	Glu	Leu	Val	Asn	
	1065				1070					1075				1080						
	Gln	Gly	Gln	Ala	Leu	Glu	Pro	Lys	Gln	Asp	Ala	Phe	Gln	Gly	Gln	Glu	Ala	Ala	Val	
				1085					1090					1095					1100	
70	Met	Met	Asp	Gln	Lys	Ala	Gly	Leu	Tyr	Gly	Gln	Thr	Tyr	Pro	Ala	Gln	Gly	Pro	Pro	
				1105					1110					1115					1120	

Met Gln Gly Gly Phe His Leu Gln Gly Gln Ser Pro Ser Phe Asn Ser Met Met Asn
 1125 1130 1135
 1140
 5 Gln Met Asn Gln Gln Gly Asn Phe Pro Leu Gln Gly Met His Pro Arg Ala Asn Ile
 1145 1150 1155
 Met Arg Pro Arg Thr Asn Thr Pro Lys Gln Leu Arg Met Gln Leu Gln Gln Arg Leu
 1160 1165 1170 1175
 Gln Gly Gln Gln Phe Leu Asn Gln Ser Arg Gln Ala Leu Glu Leu Lys Met Glu Asn
 1180 1185 1190 1195
 10 Pro Thr Ala Gly Gly Ala Ala Val Met Arg Pro Met Met Gln Pro Gln Gln Gly Phe
 1200 1205 1210 1215
 Leu Asn Ala Gln Met Val Ala Gln Arg Ser Arg Glu Leu Ser His His Phe Arg
 1220 1225 1230
 1235
 15 Gln Gln Arg Val Ala Met Met Met Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 1240 1245 1250
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Thr
 1255 1260 1265 1270
 20 Gln Ala Phe Ser Pro Pro Asn Val Thr Ala Ser Pro Ser Met Asp Gly Leu Leu
 1275 1280 1285 1290
 Ala Gly Pro Thr Met Pro Gln Ala Pro Pro Gln Gln Phe Pro Tyr Gln Pro Asn Tyr
 1295 1300 1305 1310
 Gly Met Gly Gln Gln Pro Asp Pro Ala Phe Gly Arg Val Ser Ser Pro Pro Asn Ala
 1315 1320 1325 1330
 25 Met Met Ser Ser Arg Met Gly Pro Ser Gln Asn Pro Met Met Gln His Pro Gln Ala
 1335 1340 1345
 Ala Ser Ile Tyr Gln Ser Ser Glu Met Lys Gly Trp Pro Ser Gly Asn Leu Ala Arg
 1350 1355 1360 1365
 30 Asn Ser Ser Phe Ser Gln Gln Gln Phe Ala His Gln Gly Asn Pro Ala Val Tyr Ser
 1370 1375 1380 1385
 Met Val His Met Asn Gly Ser Ser Gly His Met Gly Gln Met Asn Met Asn Pro Met
 1390 1395 1400 1405
 Pro Met Ser Gly Met Pro Met Gly Pro Asp Gln Lys Tyr Cys ***
 1410 1415 1420

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22

(B) TYPE: nucleotides

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

5'-TCATCACTTCCGACAACAGAGG-3'

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20

(B) TYPE: nucleotides

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5'-CCAGAAACGTCACTATCAAG-3'

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19

(B) TYPE: nucleotides

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

5'-TTACTGGAACCCCCATACC-3'

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 950

(B) TYPE: amino acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10	Cys	Ile	Gln	Arg	Phe	Phe	Ser	Leu	Asn	Asp	Gly	Gln	Ser	Trp	Ser	Gln	Lys	Arg	His
	1				5					10				15					
	Tyr	Gln	Glu	Ala	Tyr	Leu	Asn	Gly	His	Ala	Glu	Thr	Pro	Val	Tyr	Arg	Phe	Ser	Leu
	20				25					30					35				
	Ala	Asp	Gly	Thr	Ile	Val	Thr	Ala	Gln	Thr	Lys	Ser	Lys	Leu	Phe	Arg	Asn	Pro	Val
	40				45					50					55				
15	Thr	Asn	Asp	Arg	His	Gly	Phe	Val	Ser	Thr	His	Phe	Leu	Gln	Arg	Glu	Gln	Asn	Gly
	60				65					70					75				
	Tyr	Arg	Pro	Asn	Pro	Asn	Pro	Val	Gly	Gln	Gly	Ile	Arg	Pro	Pro	Met	Ala	Gly	Cys
	80				85					90					95				
20	Asn	Ser	Ser	Val	Gly	Gly	Met	Ser	Met	Ser	Pro	Asn	Gln	Gly	Leu	Gln	Met	Pro	Ser
	100				105					110					115				
	Ser	Arg	Ala	Tyr	Gly	Leu	Ala	Asp	Pro	Ser	Thr	Thr	Gly	Gln	Met	Ser	Gly	Ala	Arg
	120				125					130					135				
	Tyr	Gly	Gly	Ser	Ser	Asn	Ile	Ala	Ser	Leu	Thr	Pro	Gly	Pro	Gly	Met	Gln	Ser	Pro
	140				145					150					155				
25	Ser	Ser	Tyr	Gln	Asn	Asn	Asn	Tyr	Gly	Leu	Asn	Met	Ser	Ser	Pro	Pro	His	Gly	Ser
	160				165					170					175				
	Pro	Gly	Leu	Ala	Pro	Asn	Gln	Gln	Asn	Ile	Met	Ile	Ser	Pro	Arg	Asn	Arg	Gly	Ser
	180				185					190					195				
30	Pro	Lys	Ile	Ala	Ser	His	Gln	Phe	Ser	Pro	Val	Ala	Gly	Val	His	Ser	Pro	Met	Ala
	200				205					210					215				
	Ser	Ser	Gly	Asn	Thr	Gly	Asn	His	Ser	Phe	Ser	Ser	Ser	Ser	Leu	Ser	Ala	Leu	Gln
	220				225					230					235				
	Ala	Ile	Ser	Glu	Gly	Val	Gly	Thr	Ser	Leu	Leu	Ser	Thr	Leu	Ser	Ser	Pro	Gly	Pro
	240				245					250					255				
35	Lys	Leu	Asp	Asn	Ser	Pro	Asn	Met	Asn	Ile	Thr	Gln	Pro	Ser	Lys	Val	Ser	Asn	Gln
	260				265					270					275				
	Asp	Ser	Lys	Ser	Pro	Leu	Gly	Phe	Tyr	Cys	Asp	Gln	Asn	Pro	Val	Glu	Ser	Ser	Met
	280				285					290					295				
40	Cys	Gln	Ser	Asn	Ser	Arg	Asp	His	Leu	Ser	Asp	Lys	Glu	Ser	Lys	Glu	Ser	Ser	Val
	300				305					310					315				
	Glu	Gly	Ala	Glu	Asn	Gln	Arg	Gly	Pro	Leu	Glu	Ser	Lys	Gly	His	Lys	Lys	Leu	Leu
	320				325					330					335				
	Gln	Leu	Leu	Thr	Cys	Ser	Asp	Asp	Arg	Gly	His	Ser	Ser	Leu	Thr	Asn	Ser	Pro	
45	Leu	Asp	Ser	Ser	Cys	Lys	Glu	Ser	Ser	Val	Ser	Val	Thr	Ser	Pro	Ser	Gly	Val	Ser
	340				345					350					355				
	Ser	Ser	Thr	Ser	Gly	Gly	Val	Ser	Ser	Thr	Ser	Asn	Met	His	Gly	Ser	Leu	Leu	Gln
	360				365					370					375				
50	Glu	Lys	His	Arg	Ile	Leu	His	Lys	Leu	Leu	Gln	Asn	Gly	Asn	Ser	Pro	Ala	Glu	Val
	380				385					390					395				
	Ala	Lys	Ile	Thr	Ala	Glu	Ala	Thr	Gly	Lys	Asp	Thr	Ser	Ser	Ile	Thr	Ser	Cys	Gly
	400				405					410					415				
	Asp	Gly	Asn	Val	Val	Lys	Gln	Glu	Gln	Leu	Ser	Pro	Lys	Lys	Lys	Glu	Asn	Asn	Ala
	420				425					430					435				
55	Leu	Leu	Arg	Tyr	Leu	Leu	Asp	Arg	Asp	Asp	Pro	Ser	Asp	Ala	Leu	Ser	Lys	Glu	Leu
	440				445					450					455				
	Gln	Pro	Gln	Val	Glu	Gly	Val	Asp	Asn	Lys	Met	Ser	Gln	Cys	Thr	Ser	Ser	Thr	Ile
	460				465					470					475				
60	Pro	Ser	Ser	Ser	Gln	Glu	Lys	Asp	Pro	Lys	Ile	Lys	Thr	Glu	Thr	Ser	Glu	Glu	Gly
	480				485					490					495				
	Ser	Gly	Asp	Leu	Asp	Asn	Leu	Asp	Ala	Ile	Leu	Gly	Asp	Leu	Thr	Ser	Ser	Asp	Phe
	500				505					510					515				
	Tyr	Asn	Asn	Ser	Ile	Ser	Ser	Asn	Gly	Ser	His	Leu	Gly	Thr	Lys	Gln	Gln	Val	Phe
	520				525					530					535				
65	Gln	Gly	Thr	Asn	Ser	Leu	Gly	Leu	Lys	Ser	Ser	Gln	Ser	Val	Gln	Ser	Ile	Arg	Pro
	540				545					550					555				
	Pro	Tyr	Asn	Arg	Ala	Val	Ser	Leu	Asp	Ser	Pro	Val	Ser	Val	Gly	Ser	Ser	Pro	Pro
	560				565					570					575				

Val Lys Asn Ile Ser Ala Phe Pro Met Leu Pro Lys Gln Pro Met Leu Gly Gly Asn
575 580 585
Pro Arg Met Met Asp Ser Gln Glu Asn Tyr Gly Ser Ser Met Gly Gly Pro Asn Arg
590 595 600
5 Asn Val Thr Val Thr Gln Thr Pro Ser Ser Gly Asp Trp Gly Leu Pro Asn Ser Lys
610 615 620 625
Ala Gly Arg Met Glu Pro Met Asn Ser Asn Ser Met Gly Arg Pro Gly Gly Asp Tyr
630 635 640 645
10 Asn Thr Ser Leu Pro Arg Pro Ala Leu Gly Gly Ser Ile Pro Thr Leu Pro Leu Arg
650 655 660 665
Ser Asn Ser Ile Pro Gly Ala Arg Pro Val Leu Gln Gln Gln Gln Gln Met Leu Gln
670 675 680
Met Arg Pro Gly Glu Ile Pro Met Gly Met Gly Ala Asn Pro Tyr Gly Gln Ala Ala
685 690 695 700
15 Ala Ser Asn Gln Leu Gly Ser Trp Pro Asp Gly Met Leu Ser Met Glu Gln Val Ser
705 710 715 720
His Gly Thr Gln Asn Arg Pro Leu Leu Arg Asn Ser Leu Asp Asp Leu Val Gly Pro
725 730 735 740
20 Pro Ser Asn Leu Glu Gly Gln Ser Asp Glu Arg Ala Leu Leu Asp Gln Leu His Thr
745 750 755 760
Leu Leu Ser Asn Thr Asp Ala Thr Gly Leu Glu Glu Ile Asp Arg Ala Leu Gly Ile
765 770 775
Pro Glu Leu Val Asn Gln Gly Gln Ala Leu Glu Pro Lys Gln Asp Ala Phe Gln Gly
780 785 790 795
25 Gln Glu Ala Ala Val Met Asp Gln Lys Ala Gly Leu Tyr Gly Gln Thr Tyr Pro
800 805 810 815
Ala Gln Gly Pro Pro Met Gln Gly Gly Phe His Leu Gln Gly Gln Ser Pro Ser Phe
820 825 830 835
30 Asn Ser Met Met Asn Gln Met Asn Gln Gln Gly Asn Phe Pro Leu Gln Gly Met His
840 845 850 855
Pro Arg Ala Asn Ile Met Arg Pro Arg Thr Asn Thr Pro Lys Gln Leu Arg Met Gln
860 865 870
Leu Gln Gln Arg Leu Gln Gly Gln Gln Phe Leu Asn Gln Ser Arg Gln Ala Leu Glu
875 880 885 890
35 Leu Lys Met Glu Asn Pro Thr Ala Gly Gly Ala Ala Val Met Arg Pro Met Met Gln
895 900 905 910
Pro Gln Gln Gly Phe Leu Asn Ala Gln Met Val Ala Gln Arg Ser Arg Glu Leu Leu
915 920 925 930
40 Ser His His Phe Arg Gln Gln Arg Val Ala Met Met Met Gln Gln Gln Gln Gln Gln
935 940 945 950
Gln

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4621 nucleotides; 1539 amino acid residues
(B) TYPE: mouse DNA and amino acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

50
G GCG GCG AAC GGA TCA AAA GAA TTT GCT GAA CAG TGG ACT CCG AGA TCG GTA AAA
1 5 10 15
CGA ACT CTT CCC TGC CCT TCC TGA ACA GCT GTC AGT TGC TGA TCT GTG ATC AGG
20 25 30 35
55 ATG AGT GGA CTA GGC GAA AGC TCT TTG GAT CCG CTG GCC GCT GAG TCT CGG AAA
Met Ser Gly Leu Gly Glu Ser Ser Leu Asp Pro Leu Ala Ala Glu Ser Arg Lys
40 45 50 55
CGC AAA CTG CCC TGT GAT GCC CCA GGA CAG GGG CTT GTC TAC AGT GGT GAG AAG
Arg Lys Leu Pro Cys Asp Ala Pro Gly Gln Gly Leu Val Tyr Ser Gly Glu Lys
60 65 70
TGG CGA CGG GAG CAG GAG AGC AAG TAC ATA GAG GAG CTG GCA GAG CTC ATC TCT
Trp Arg Arg Glu Gln Glu Ser Lys Tyr Ile Glu Glu Leu Ala Glu Leu Ile Ser
75 80 85 90
65 GCA AAT CTC AGC GAC ATC GAC AAC TTC AAT GTC AAG CCA GAT AAA TGT GCC ATC
Ala Asn Leu Ser Asp Ile Asp Asn Phe Asn Val Lys Pro Asp Lys Cys Ala Ile
95 100 105
CTA AAG GAG ACA GTG AGA CAG ATA CGG CAA ATA AAA GAA CAA GGA AAA ACT ATT
Leu Lys Glu Thr Val Arg Gln Ile Arg Gln Ile Lys Glu Gln Gly Lys Thr Ile
110 115 120 125

TCC AGT GAT GAT GAT GTT CAA AAA GCT GAT GTG TCT TCT ACA GGG CAG GGA GTC
 Ser Ser Asp Asp Asp Val Gln Lys Ala Asp Val Ser Ser Thr Gly Gln Gly Val
 130 135 140 145
 5 ATT GAT AAA GAC TCT TTA GGA CCG CTT TTA CTA CAG GCA CTG GAT GGT TTC CTG
 Ile Asp Lys Asp Ser Leu Gly Pro Leu Leu Leu Gln Ala Leu Asp Gly Phe Leu
 150 155 160
 TTT GTG GTG AAT CGA GAT GGA AAC ATT GTA TTC GTG TCA GAA AAT GTC ACA CAG
 Phe Val Val Asn Arg Asp Gly Asn Ile Val Phe Val Ser Glu Asn Val Thr Gln
 165 170 175 180
 10 TAT CTG CAG TAC AAG CAG GAG GAC CTG GTT AAC ACA AGT GTC TAC AGC ATC TTA
 Tyr Leu Gln Tyr Lys Gln Glu Asp Leu Val Asn Thr Ser Val Tyr Ser Ile Leu
 185 190 195
 CAT GAG CAA GAC CGG AAG GAT TTT CTT AAA CAC TTA CCA AAA TCC ACA GTT AAT
 His Glu Gln Asp Arg Lys Asp Phe Leu Lys His Leu Pro Lys Ser Thr Val Asn
 200 205 210 215
 15 GGA GTT TCT TGG ACT AAT GAG AAC CAG AGA CAA AAA AGC CAT ACA TTT AAT TGT
 Gly Val Ser Trp Thr Asn Glu Asn Gln Arg Gln Lys Ser His Thr Phe Asn Cys
 220 225 230 235
 20 CGT ATG TTG ATG AAA ACA CAC GAC ATT TTG GAA GAC GTG AAT GCC AGT CCC GAA
 Arg Met Leu Met Lys Thr His Asp Ile Leu Glu Asp Val Asn Ala Ser Pro Glu
 240 245 250
 ACA CGC CAG AGA TAT GAA ACA ATG CAG TGC TTT GCC CTG TCT CAG CCT CGC GCT
 Thr Arg Gln Arg Tyr Glu Thr Met Gln Cys Phe Ala Leu Ser Gln Pro Arg Ala
 255 260 265 270
 25 ATG CTG GAA GAA GGA GAA GAC TTG CAG TGC TGT ATG ATC TGC GTG GCT CGC CGC
 Met Leu Glu Glu Gly Glu Asp Leu Gln Cys Cys Met Ile Cys Val Ala Arg Arg
 275 280 285
 GTG ACT GCG CCA TTC CCA TCC AGT CCT GAG AGC TTT ATT ACC AGA CAT GAC CTT
 Val Thr Ala Pro Phe Pro Ser Ser Pro Glu Ser Phe Ile Thr Arg His Asp Leu
 290 295 300 305
 30 TCC GGA AAG GTT GTC AAT ATA GAT ACA AAC TCA CTT AGA TCT TCC ATG AGG CCT
 Ser Gly Lys Val Val Asn Ile Asp Thr Asn Ser Leu Arg Ser Ser Met Arg Pro
 310 315 320 325
 35 GGC TTT GAA GAC ATA ATC CGA AGA TGT ATC CAG AGG TTC TTC AGT CTG AAT GAT
 Gly Phe Glu Asp Ile Ile Arg Arg Cys Ile Gln Arg Phe Phe Ser Leu Asn Asp
 330 335 340
 GGG CAG TCA TGG TCC CAG AAG CGT CAC TAT CAA GAA GCT TAT GTT CAT GGC CAC
 Gly Gln Ser Trp Ser Gln Lys Arg His Tyr Gln Glu Ala Tyr Val His Gly His
 345 350 355 360
 40 GCA GAG ACC CCC GTG TAT CGT TTC TCC TTG GCT GAT GGA ACT ATT GTG AGT GCG
 Ala Glu Thr Pro Val Tyr Arg Phe Ser Leu Ala Asp Gly Thr Ile Val Ser Ala
 365 370 375
 CAG ACA AAA AGC AAA CTC TTC CGC AAT CCT GTA ACG AAT GAT CGT CAC GGC TTC
 Gln Thr Lys Ser Lys Leu Phe Arg Asn Pro Val Thr Asn Asp Arg His Gly Phe
 380 385 390 395
 45 ATC TCG ACC CAC TTT CTT CAG AGA GAA CAG AAT GGA TAC AGA CCA AAC CCA AAT
 Ile Ser Thr His Phe Leu Gln Arg Glu Gln Asn Gly Tyr Arg Pro Asn Pro Asn
 400 405 410 415
 50 CCC GCA GGA CAA GGC ATC CGA CCT CCT GCA GCA GGG TGT GGC GTG AGC ATG TCT
 Pro Ala Gly Gln Gly Ile Arg Pro Pro Ala Ala Gly Cys Gly Val Ser Met Ser
 420 425 430
 55 CCA AAT CAG AAT GTA CAG ATG ATG GGC AGC CGG ACC TAT GGC GTG CCA GAC CCC
 Pro Asn Gln Asn Val Gln Met Met Gly Ser Arg Thr Tyr Gly Val Pro Asp Pro
 435 440 445 450
 AGC AAC ACA GGG CAG ATG GGT GGA GCT AGG TAC GGG GCT TCT AGT AGC GTA GCC
 Ser Asn Thr Gly Gln Met Gly Gly Ala Arg Tyr Gly Ala Ser Ser Val Ala
 455 460 465
 60 TCA CTG ACG CCA GGA CAA AGC CTA CAG TCG CCA TCT TCC TAT CAG AAC AGC AGC
 Ser Leu Thr Pro Gly Gln Ser Leu Gln Ser Pro Ser Ser Tyr Gln Asn Ser Ser
 470 475 480 485
 TAT GGG CTC AGC ATG AGC AGT CCC CCC CAC GGC AGT CCT GGT CTT GGT CCC AAC
 Tyr Gly Leu Ser Met Ser Ser Pro Pro His Gly Ser Pro Gly Leu Gly Pro Asn
 490 495 500 505
 65 CAG CAG AAC ATC ATG ATT TCC CCT CGG AAT CGT GGC AGC CCA AAG ATG GCC TCC
 Gln Gln Asn Ile Met Ile Ser Pro Arg Asn Arg Gly Ser Pro Lys Met Ala Ser
 510 515 520
 70 CAC CAG TTC TCT CCT GCT GCA GGT GCA CAC TCA CCC ATG GGA CCT TCT GGC AAC
 His Gln Phe Ser Pro Ala Ala Gly Ala His Ser Pro Met Gly Pro Ser Gly Asn
 525 530 535 540

	ACA	GGG	AGC	CAC	AGC	TTT	TCT	AGC	AGC	TCC	CTC	AGT	GCC	TTG	CAA	GCC	ATC	AGT
	Thr	Gly	Ser	His	Ser	Phe	Ser	Ser	Ser	Ser	Leu	Ser	Ala	Leu	Gln	Ala	Ile	Ser
				545					550					555				
5	GAA	GGC	GTG	GGG	ACC	TCT	CTT	TTA	TCT	ACT	CTG	TCC	TCA	CCA	GGC	CCC	AAA	CTG
	Glu	Gly	Val	Gly	Thr	Ser	Leu	Leu	Ser	Thr	Leu	Ser	Ser	Pro	Gly	Pro	Lys	Leu
	560			565					570						575			
	GAT	AAT	TCT	CCC	AAT	ATG	Asn	ATA	AGC	CAG	CCA	AGT	AAA	GTG	AGT	GGT	CAG	GAC
	Asp	Asn	Ser	Pro	Asn	Met	Asn	Ile	Ser	Gln	Pro	Ser	Lys	Val	Ser	Gly	Gln	Asp
				580				585					590					595
10	TCT	AAG	AGC	CCC	CTA	GGC	TTA	TAC	TGT	GAA	CAG	AAT	CCA	GTG	GAG	AGT	TCA	GTG
	Ser	Lys	Ser	Pro	Leu	Gly	Leu	Tyr	Cys	Glu	Gln	Asn	Pro	Val	Glu	Ser	Ser	Val
				600					605					610				
	TGT	CAG	TCA	AAC	AGC	AGA	GAT	CAC	CCA	AGT	GAA	AAA	GAA	AGC	AAG	GAG	AGC	AGT
	Cys	Gln	Ser	Asn	Ser	Arg	Asp	His	Pro	Ser	Glu	Lys	Glu	Ser	Lys	Glu	Ser	Ser
	615					620						625					630	
15	GGG	GAG	GTG	TCA	GAG	ACG	CCC	AGG	GGA	CCT	CTG	GAA	AGC	AAA	GGC	CAC	AAG	AAA
	Gly	Glu	Val	Ser	Glu	Thr	Pro	Arg	Gly	Pro	Leu	Glu	Ser	Lys	Gly	His	Lys	Lys
				635				640					645					
20	CTG	CTG	CAG	TTA	CTC	ACG	TGC	TCC	TCC	GAC	ASP	CGA	GGC	CAT	TCC	TCC	TTG	ACC
	Leu	Leu	Gln	Leu	Leu	Thr	Cys	Ser	Ser	Asp	Arg	Gly	His	Ser	Ser	Leu	Thr	
	650					655				660					665			
	AAC	TCT	CCC	CTG	GAT	CCA	AAC	TGC	AAA	GAC	TCT	TCC	GTT	AGT	GTC	ACC	AGC	CCC
	Asn	Ser	Pro	Leu	Asp	Pro	Asn	Cys	Lys	Asp	Ser	Ser	Val	Ser	Val	Thr	Ser	Pro
				670				675					680					685
25	TCT	GGA	GTG	TCC	TCC	TCA	ACA	TCA	GGG	ACA	GTG	TCT	TCC	ACC	TCC	AAT	GTG	CAT
	Ser	Gly	Val	Ser	Ser	Ser	Thr	Ser	Gly	Thr	Val	Ser	Ser	Thr	Ser	Asn	Val	His
					690				695					700				
	GGG	TCT	CTG	TTG	CAA	GAG	AAA	CAC	CGG	ATT	TTG	CAC	AAG	TTG	CTG	CAG	AAT	GGC
	Gly	Ser	Leu	Leu	Gln	Glu	Lys	His	Arg	Ile	Leu	His	Lys	Leu	Leu	Gln	Asn	Gly
	705				710				715					720				
30	AAC	TCC	CCA	GCG	GAG	GTC	GCC	AAG	ATC	ACT	GCA	GAG	GCC	ACT	GGG	AAG	GAC	ACG
	Asn	Ser	Pro	Ala	Glu	Val	Ala	Lys	Ile	Thr	Ala	Glu	Ala	Thr	Gly	Lys	Asp	Thr
				725				730					735					740
35	AGC	AGC	ACT	GCT	TCC	TGT	GGA	GAG	GGG	ACA	ACC	AGG	CAG	GAG	CAG	CTG	AGT	CCT
	Ser	Ser	Thr	Ala	Ser	Cys	Gly	Glu	Gly	Thr	Thr	Arg	Gln	Glu	Gln	Leu	Ser	Pro
					745				750					755				
	AAG	AAG	AAG	GAG	AAT	AAT	GCT	CTG	CTT	AGA	TAC	CTG	CTG	GAC	AGG	GAT	GAC	CCC
	Lys	Lys	Lys	Glu	Asn	Asn	Ala	Leu	Leu	Arg	Tyr	Leu	Leu	Asp	Arg	Asp	Asp	Pro
				760			765				770			775				
40	AGT	GAT	GTG	CTT	GCC	AAA	GAG	CTG	CAG	CCC	CAG	GCC	GAC	AGT	GGG	GAC	AGT	AAA
	Ser	Asp	Val	Leu	Ala	Lys	Glu	Leu	Gln	Pro	Gln	Ala	Asp	Ser	Gly	Asp	Ser	Lys
				780				785					790					
45	CTG	AGT	CAG	TGC	AGC	TGC	TCC	ACC	AAT	CCC	AGC	TCT	GGC	CAA	GAG	AAA	GAC	CCC
	Leu	Ser	Gln	Cys	Ser	Cys	Ser	Thr	Asn	Pro	Ser	Ser	Gly	Gln	Glu	Lys	Asp	Pro
	795					800					805					810		
	AAA	ATT	AAG	ACC	GAG	ACG	AAC	GAG	GAG	GTA	TCG	GGA	GAC	CTG	GAT	AAT	CTA	GAT
	Lys	Ile	Lys	Thr	Glu	Thr	Asn	Glu	Glu	Val	Ser	Gly	Asp	Leu	Asp	Asn	Leu	Asp
				815				820					825					830
50	GCC	ATT	CTT	GGA	GAT	TTG	ACC	AGT	TCT	GAC	TTC	TAC	AAC	AAT	CCT	ACA	AAT	GGC
	Ala	Ile	Leu	Gly	Asp	Leu	Thr	Ser	Ser	Asp	Phe	Tyr	Asn	Asn	Pro	Thr	Asn	Gly
					835				840					845				
	GGT	CAC	CCA	GGG	GCC	AAA	CAG	CAG	ATG	TTT	GCA	GGA	CCG	AGT	TCT	CTG	GGT	TTG
	Gly	His	Pro	Gly	Ala	Lys	Gln	Gln	Met	Phe	Ala	Gly	Pro	Ser	Ser	Leu	Gly	Leu
				850			855				860					865		
55	CGA	AGT	CCA	CAG	CCT	GTG	CAG	TCT	GTT	CGT	CCT	CCA	TAT	AAC	CGA	GCG	GTG	TCT
	Arg	Ser	Pro	Gln	Pro	Val	Gln	Ser	Val	Arg	Pro	Pro	Tyr	Asn	Arg	Ala	Val	Ser
				870				875					880					
60	CTG	GAT	AGC	CCT	GTG	TCT	GTT	GGC	TCA	GGT	CCG	CCA	GTG	AAG	AAT	GTC	AGT	GCT
	Leu	Asp	Ser	Pro	Val	Ser	Val	Gly	Ser	Gly	Pro	Pro	Val	Lys	Asn	Val	Ser	Ala
						890					895				900			
	TTC	CCT	GGG	TTA	CCA	AAA	CAG	CCC	ATA	CTG	GCT	GGG	AAT	CCA	AGA	ATG	ATG	GAT
	Phe	Pro	Gly	Leu	Pro	Lys	Gln	Pro	Ile	Leu	Ala	Gly	Asn	Pro	Arg	Met	Met	Asp
				905			910						915			920		
65	AGT	CAG	GAG	AAT	TAC	GGT	GCC	AAC	ATG	GGC	CCA	AAC	AGA	AAT	GTT	CCT	GTG	AAT
	Ser	Gln	Glu	Asn	Tyr	Gly	Ala	Asn	Met	Gly	Pro	Asn	Arg	Asn	Val	Pro	Val	Asn
				925			930						935					
	CCG	ACT	TCC	TCC	CCC	GGA	GAC	TGG	GGC	TTA	GCT	AAC	TCA	AGG	GCC	AGC	AGA	ATG
	Pro	Thr	Ser	Ser	Pro	Gly	Asp	Trp	Gly	Leu	Ala	Asn	Ser	Arg	Ala	Ser	Arg	Met
						945					950				955			
70	GAG	CCT	CTG	GCA	TCA	AGT	CCC	CTG	GGA	AGA	ACT	GGA	GCC	GAT	TAC	AGT	GCC	ACT

Glu Pro Leu Ala Ser Ser Pro Leu Gly Arg Thr Gly Ala Asp Tyr Ser Ala Thr
 960 965 970 975
 TTA CCC AGA CCT GCC ATG GGG GGC TCT GTG CCT ACC TTG CCA CTT CGT TCT AAT
 Leu Pro Arg Pro Ala Met Gly Ser Val Pro Thr Leu Pro Leu Arg Ser Asn
 980 985 990
 CGA CTG CCA GGT GCA AGA CCA TCG TTG CAG CAA CAG CAG CAG CAA CAG CAG CAA
 Arg Leu Pro Gly Ala Arg Pro Ser Leu Gln Gln Gln Gln Gln Gln Gln Gln
 995 1000 1005 1010
 CAG CAA CAA CAA CAG CAG CAA CAG CAG CAG CAA CAG CAG CAG CAG CAA CAG CAG
 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 1015 1020 1025
 CAG ATG CTT CAA ATG AGA ACT GGT GAG ATT CCC ATG GGA ATG GGA GTC AAT CCC
 Gln Met Leu Gln Met Arg Thr Gly Glu Ile Pro Met Gly Met Gly Val Asn Pro
 1030 1035 1040 1045
 TAT AGC CCA GCA GTG CCG TCT AAC CAA CCA GGT TCC TGG CCA GAG GGC ATG CTC
 Tyr Ser Pro Ala Val Pro Ser Asn Gln Pro Gly Ser Trp Pro Glu Gly Met Leu
 1050 1055 1060 1065
 TCT ATG GAA CAA GGT CCT CAC GGG TCT CAA AAT AGG CCT CTT CTT AGA AAC TCT
 Ser Met Glu Gln Gln Pro His Gly Ser Gln Asn Arg Pro Leu Leu Arg Asn Ser
 1070 1075 1080
 CTG GAT GAT CTG CTT GGG CCA CCT TCT AAC GCA GAG GGC CAG AGT GAC GAG AGA
 Leu Asp Asp Leu Leu Gly Pro Pro Ser Asn Ala Glu Gly Gln Ser Asp Glu Arg
 1085 1090 1095 1100
 GCT CTG CTG GAC CAG CTG CAC ACA CTC CTG AGC AAC ACA GAT GCC ACA GGT CTG
 Ala Leu Leu Asp Gln Leu His Thr Leu Leu Ser Asn Thr Asp Ala Thr Gly Leu
 1105 1110 1115
 GAG GAG ATC GAC AGG GCC TTG GGA ATT CCT GAG CTC GTG AAT CAG GGA CAA GCT
 Glu Glu Ile Asp Arg Ala Leu Gly Ile Pro Glu Leu Val Asn Gln Gly Gln Ala
 1120 1125 1130 1135
 TTG GAG TCC AAA CAG GAT GTT TTC CAA GGC CAA GAA GCA GCA GTA ATG ATG GAT
 Leu Glu Ser Lys Gln Asp Val Phe Gln Gly Gln Glu Ala Ala Val Met Met Asp
 1140 1145 1150 1155
 CAG AAG GCT GCA CTA TAT GGA CAG ACA TAC CCA GCT CAG GGT CCT CCC CTT CAA
 Gln Lys Ala Ala Leu Tyr Gly Gln Thr Tyr Pro Ala Gln Gly Pro Pro Leu Gln
 1160 1165 1170
 GGA GGC TTT AAC CTT CAG GGA CAG TCA CCA TCG TTT AAC TCT ATG ATG GGT CAG
 Gly Gly Phe Asn Leu Gln Gly Gln Ser Pro Ser Phe Asn Ser Met Met Gly Gln
 1175 1180 1185 1190
 ATT AGC CAG CAA GGC AGC TTT CCT CTG CAA GGC ATG CAT CCT AGA GCC GGC CTC
 Ile Ser Gln Gln Gly Ser Phe Pro Leu Gln Gly Met His Pro Arg Ala Gly Leu
 1195 1200 1205
 GTG AGA CCA AGG ACC AAC ACC CCG AAG CAG CTG AGA ATG CAG CTT CAG CAG AGG
 Val Arg Pro Arg Thr Asn Thr Pro Lys Gln Leu Arg Met Gln Leu Gln Gln Arg
 1210 1215 1220 1225
 CTA CAG GGC CAG CAG TTT TTA AAT CAG AGC CGG CAG GCA CTT GAA ATG AAA ATG
 Leu Gln Gly Gln Gln Phe Leu Asn Gln Ser Arg Gln Ala Leu Glu Met Lys Met
 1230 1235 1240 1245
 GAG AAC CCT GCT GGC ACT GCT GTG ATG AGG CCC ATG ATG CCC CAG GCT TTC TTT
 Glu Asn Pro Ala Gly Thr Ala Val Met Arg Pro Met Met Pro Gln Ala Phe Phe
 1250 1255 1260
 AAT GCC CAA ATG GCT GCC CAG CAG AAA CGA GAG CTG ATG AGC CAT CAC CTG CAG
 Asn Ala Gln Met Ala Ala Gln Gln Lys Arg Glu Leu Met Ser His His Leu Gln
 1265 1270 1275 1280
 CAG CAG AGG ATG GCG ATG ATG ATG TCA CAA CCA CAG CCT CAG GCC TTC AGC CCA
 Gln Gln Arg Met Ala Met Met Met Ser Gln Pro Gln Pro Gln Ala Phe Ser Pro
 1285 1290 1295
 CCT CCC AAC GTC ACC GCC TCC CCC AGC ATG GAC GGG GTT TTG GCA GGT TCA GCA
 Pro Pro Asn Val Thr Ala Ser Pro Ser Met Asp Gly Val Leu Ala Gly Ser Ala
 1300 1305 1310 1315
 ATG CCG CAA GCC CCT CCA CAA CAG TTT CCA GCA AAT TAC GGA ATG GGA
 Met Pro Gln Ala Pro Pro Gln Gln Phe Pro Tyr Pro Ala Asn Tyr Gly Met Gly
 1320 1325 1330 1335
 CAA CCA CCA GAG CCA GCC TTT GGT CGA GGC TCG AGT CCT CCC AGT GCA ATG ATG
 Gln Pro Pro Glu Pro Ala Phe Gly Arg Gly Ser Ser Pro Pro Ser Ala Met Met
 1340 1345 1350
 TCA TCA AGA ATG GGG CCT TCC CAG AAT GCC ATG GTG CAG CAT CCT CAG CCC ACA
 Ser Ser Arg Met Gly Pro Ser Gln Asn Ala Met Val Gln His Pro Gln Pro Thr
 1355 1360 1365 1370
 CCC ATG TAT CAG CCT TCA GAT ATG AAG GGG TGG CCG TCA GGG AAC CTG GCC AGG
 Pro Met Tyr Gln Pro Ser Asp Met Lys Gly Trp Pro Ser Gly Asn Leu Ala Arg

1375 1380 1385
 AAT GGC TCC TTC CCC CAG CAG CAG TTT GCT CCC CAG GGG AAC CCT GCA GCC TAC
 Asn Gly Ser Phe Pro Gln Gln Phe Ala Pro Gln Gly Asn Pro Ala Ala Tyr
 1390 1395 1400 1405
 5 AAC ATG GTG CAT ATG AAC AGC AGC GGT GGG CAC TTG GGA CAG ATG GCC ATG ACC
 Asn Met Val His Met Asn Ser Ser Gly Gly His Leu Gly Gln Met Ala Met Thr
 1410 1415 1420
 CCC ATG CCC ATG TCT GGC ATG CCC ATG GGC CCC GAT CAG AAA TAC TGC TGA CAT
 Pro Met Pro Met Ser Gly Met Pro Met Gly Pro Asp Gln Lys Tyr Cys *** His
 1425 1430 1435 1440
 CTC CCT AGT GGG ACT GAC TGT ACA GAT GAC ACT GCA CAG GAT CAT CAG GAC GTG
 Leu Pro Ser Gly Thr Asp Cys Thr Asp Asp Thr Ala Gln Asp His Gln Asp Val
 1445 1450 1455
 15 GCG GCG AGT CAT TGT CTA AGC ATC CAG CTT GGA AAC AAG GCC AGC GTG ACC AGC
 Ala Ala Ser His Cys Leu Ser Ile Gln Leu Gly Asn Lys Ala Ser Val Thr Ser
 1460 1465 1470 1475
 AGC GGG GTC TGT GCT GTC ATT TGA GCA GAG CTG GGT CTC GCT GAA GCG CAC TGT
 Ser Gly Val Cys Ala Val Ile ***
 1480 1485 1490 1495
 20 CTA CCT GAT GCC CTG CCT CTG TGT GGC AAG GTG TTC TGC CTC ATG AGG ATG TGA
 1500 1505 1510
 TTC TGG AGA TGG GGT GTT CGT AAG CAC CGC TCT CTT ACG TCA CTC CCT TCT GCC
 1515 1520 1525 1530
 25 TCG CCA GCC AAA GTC TTC ACG TAG ATC TAG
 1535 1540

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

5'-TCCTTTTCCCAGCAGCAGTTTG-3'

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5'ATGCCAGACATGGGCATGGG-3'

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539
 (B) TYPE: amino acid
 (C) STRANDEDNESS: Single
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

55 Met Ser Gly Leu Gly Glu Ser Ser Leu Asp Pro Leu Ala Ala Glu Ser Arg Lys
 40 45 50 55
 Arg Lys Leu Pro Cys Asp Ala Pro Gly Gln Gly Leu Val Tyr Ser Gly Glu Lys
 60 65 70
 60 Trp Arg Arg Glu Gln Glu Ser Lys Tyr Ile Glu Glu Leu Ala Glu Leu Ile Ser
 75 80 85 90
 Ala Asn Leu Ser Asp Ile Asp Asn Phe Asn Val Lys Pro Asp Lys Cys Ala Ile
 95 100 105
 Leu Lys Glu Thr Val Arg Gln Ile Arg Gln Ile Lys Glu Gln Gly Lys Thr Ile
 110 115 120 125

	Ser	Ser	Asp	Asp	Asp	Val	Gln	Lys	Ala	Asp	Val	Ser	Ser	Thr	Gly	Gln	Gly	Val
			130					135					140					145
	Ile	Asp	Lys	Asp	Ser	Leu	Gly	Pro	Leu	Leu	Gln	Ala	Leu	Asp	Gly	Phe	Leu	
				150					155					160				
5	Phe	Val	Val	Asn	Arg	Asp	Gly	Asn	Ile	Val	Phe	Val	Ser	Glu	Asn	Val	Thr	Gln
		165				170					175						180	
	Tyr	Leu	Gln	Tyr	Lys	Gln	Glu	Asp	Leu	Val	Asn	Thr	Ser	Val	Tyr	Ser	Ile	Leu
			185					190						195				
10	His	Glu	Gln	Asp	Arg	Lys	Asp	Phe	Leu	Lys	His	Leu	Pro	Lys	Ser	Thr	Val	Asn
		200				205					210					215		
	Gly	Val	Ser	Trp	Thr	Asn	Glu	Asn	Gln	Arg	Gln	Lys	Ser	His	Thr	Phe	Asn	Cys
			220				225					230					235	
	Arg	Met	Leu	Met	Lys	Thr	His	Asp	Ile	Leu	Glu	Asp	Val	Asn	Ala	Ser	Pro	Glu
				240						245					250			
15	Thr	Arg	Gln	Arg	Tyr	Glu	Thr	Met	Gln	Cys	Phe	Ala	Leu	Ser	Gln	Pro	Arg	Ala
		255				260					265						270	
	Met	Leu	Glu	Glu	Gly	Glu	Asp	Leu	Gln	Cys	Cys	Met	Ile	Cys	Val	Ala	Arg	Arg
			275				280						285					
20	Val	Thr	Ala	Pro	Phe	Pro	Ser	Ser	Pro	Glu	Ser	Phe	Ile	Thr	Arg	His	Asp	Leu
		290				295					300					305		
	Ser	Gly	Lys	Val	Val	Asn	Ile	Asp	Thr	Asn	Ser	Leu	Arg	Ser	Ser	Met	Arg	Pro
			310					315					320				325	
25	Gly	Phe	Glu	Asp	Ile	Ile	Arg	Arg	Cys	Ile	Gln	Arg	Phe	Phe	Ser	Leu	Asn	Asp
				330						335					340			
	Gly	Gln	Ser	Trp	Ser	Gln	Lys	Arg	His	Tyr	Gln	Glu	Ala	Tyr	Val	His	Gly	His
		345					350					355					360	
	Ala	Glu	Thr	Pro	Val	Tyr	Arg	Phe	Ser	Leu	Ala	Asp	Gly	Thr	Ile	Val	Ser	Ala
			365					370						375				
30	Gln	Thr	Lys	Ser	Lys	Leu	Phe	Arg	Asn	Pro	Val	Thr	Asn	Asp	Arg	His	Gly	Phe
		380				385					390					395		
	Ile	Ser	Thr	His	Phe	Leu	Gln	Arg	Glu	Gln	Asn	Gly	Tyr	Arg	Pro	Asn	Pro	Asn
			400				405					410					415	
35	Pro	Ala	Gly	Gln	Gly	Ile	Arg	Pro	Pro	Ala	Ala	Gly	Cys	Gly	Val	Ser	Met	Ser
				420					425						430			
	Pro	Asn	Gln	Asn	Val	Gln	Met	Met	Gly	Ser	Arg	Thr	Tyr	Gly	Val	Pro	Asp	Pro
		435				440					445					450		
	Ser	Asn	Thr	Gly	Gln	Met	Gly	Gly	Ala	Arg	Tyr	Gly	Ala	Ser	Ser	Ser	Val	Ala
			455				460					465						
40	Ser	Leu	Thr	Pro	Gly	Gln	Ser	Leu	Gln	Ser	Pro	Ser	Ser	Tyr	Gln	Asn	Ser	Ser
		470				475					480					485		
	Tyr	Gly	Leu	Ser	Met	Ser	Ser	Pro	Pro	His	Gly	Ser	Pro	Gly	Leu	Gly	Pro	Asn
			490				495					500					505	
45	Gln	Gln	Asn	Ile	Met	Ile	Ser	Pro	Arg	Asn	Arg	Gly	Ser	Pro	Lys	Met	Ala	Ser
				510					515						520			
	His	Gln	Phe	Ser	Pro	Ala	Ala	Gly	Ala	His	Ser	Pro	Met	Gly	Pro	Ser	Gly	Asn
		525				530					535					540		
	Thr	Gly	Ser	His	Ser	Phe	Ser	Ser	Ser	Leu	Ser	Ala	Leu	Gln	Ala	Ile	Ser	
			545					550					555					
50	Glu	Gly	Val	Gly	Thr	Ser	Leu	Leu	Ser	Thr	Leu	Ser	Ser	Ser	Gly	Pro	Lys	Leu
		560				565				570					575			
	Asp	Asn	Ser	Pro	Asn	Met	Asn	Ile	Ser	Gln	Pro	Ser	Lys	Val	Ser	Gly	Gln	Asp
			580				585					590					595	
55	Ser	Lys	Ser	Pro	Leu	Gly	Leu	Tyr	Cys	Glu	Gln	Asn	Pro	Val	Glu	Ser	Ser	Val
				600					605					610				
	Cys	Gln	Ser	Asn	Ser	Arg	Asp	His	Pro	Ser	Glu	Lys	Glu	Ser	Lys	Glu	Ser	Ser
		615				620					625					630		
	Gly	Glu	Val	Ser	Glu	Thr	Pro	Arg	Gly	Pro	Leu	Glu	Ser	Lys	Gly	His	Lys	Lys
			635				640						645					
60	Leu	Leu	Gln	Leu	Leu	Thr	Cys	Ser	Ser	Asp	Asp	Arg	Gly	His	Ser	Ser	Leu	Thr
		650				655				660					665			
	Asn	Ser	Pro	Leu	Asp	Pro	Asn	Cys	Lys	Asp	Ser	Ser	Val	Ser	Val	Thr	Ser	Pro
			670				675					680					685	
65	Ser	Gly	Val	Ser	Ser	Ser	Thr	Ser	Gly	Thr	Val	Ser	Ser	Thr	Ser	Asn	Val	His
				690					695				700					
	Gly	Ser	Leu	Leu	Gln	Glu	Lys	His	Arg	Ile	Leu	His	Lys	Leu	Leu	Gln	Asn	Gly
		705				710				715					720			
	Asn	Ser	Pro	Ala	Glu	Val	Ala	Lys	Ile	Thr	Ala	Glu	Ala	Thr	Gly	Lys	Asp	Thr
			725				730					735					740	
70	Ser	Ser	Thr	Ala	Ser	Cys	Gly	Glu	Gly	Thr	Thr	Arg	Gln	Glu	Gln	Leu	Ser	Pro
				745					750						755			

Lys Lys Lys Glu Asn Asn Ala Leu Leu Arg Tyr Leu Leu Asp Arg Asp Asp Pro
 760 765 770 775
 Ser Asp Val Leu Ala Lys Glu Leu Gln Pro Gln Ala Asp Ser Gly Asp Ser Lys
 780 785 790
 5 Leu Ser Gln Cys Ser Cys Ser Thr Asn Pro Ser Ser Gly Gln Glu Lys Asp Pro
 795 800 805 810
 Lys Ile Lys Thr Glu Thr Asn Glu Glu Val Ser Gly Asp Leu Asp Asn Leu Asp
 815 820 825 830
 10 Ala Ile Leu Gly Asp Leu Thr Ser Ser Asp Phe Tyr Asn Asn Pro Thr Asn Gly
 835 840 845
 Gly His Pro Gly Ala Lys Gln Gln Met Phe Ala Gly Pro Ser Ser Leu Gly Leu
 850 855 860 865
 Arg Ser Pro Gln Pro Val Gln Ser Val Arg Pro Pro Tyr Asn Arg Ala Val Ser
 870 875 880
 15 Leu Asp Ser Pro Val Ser Val Gly Ser Gly Pro Pro Val Lys Asn Val Ser Ala
 885 890 895 900
 Phe Pro Gly Leu Pro Lys Gln Pro Ile Leu Ala Gly Asn Pro Arg Met Met Asp
 905 910 915 920
 20 Ser Gln Glu Asn Tyr Gly Ala Asn Met Gly Pro Asn Arg Asn Val Pro Val Asn
 925 930 935
 Pro Thr Ser Ser Pro Gly Asp Trp Gly Leu Ala Asn Ser Arg Ala Ser Arg Met
 940 945 950 955
 Glu Pro Leu Ala Ser Ser Pro Leu Gly Arg Thr Gly Ala Asp Tyr Ser Ala Thr
 960 965 970 975
 25 Leu Pro Arg Pro Ala Met Gly Gly Ser Val Pro Thr Leu Pro Leu Arg Ser Asn
 980 985 990
 Arg Leu Pro Gly Ala Arg Pro Ser Leu Gln Gln Gln Gln Gln Gln Gln Gln
 995 1000 1005 1010
 30 Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
 1015 1020 1025
 Gln Met Leu Gln Met Arg Thr Gly Glu Ile Pro Met Gly Met Gly Val Asn Pro
 1030 1035 1040 1045
 Tyr Ser Pro Ala Val Pro Ser Asn Gln Pro Gly Ser Trp Pro Glu Gly Met Leu
 1050 1055 1060 1065
 35 Ser Met Glu Gln Gly Pro His Gly Ser Gln Asn Arg Pro Leu Leu Arg Asn Ser
 1070 1075 1080
 Leu Asp Asp Leu Leu Gly Pro Pro Ser Asn Ala Glu Gly Gln Ser Asp Glu Arg
 1085 1090 1095 1100
 40 Ala Leu Leu Asp Gln Leu His Thr Leu Leu Ser Asn Thr Asp Ala Thr Gly Leu
 1105 1110 1115
 Glu Glu Ile Asp Arg Ala Leu Gly Ile Pro Glu Leu Val Asn Gln Gly Gln Ala
 1120 1125 1130 1135
 Leu Glu Ser Lys Gln Asp Val Phe Gln Gly Gln Glu Ala Ala Val Met Met Asp
 1140 1145 1150 1155
 45 Gln Lys Ala Ala Leu Tyr Gly Gln Thr Tyr Pro Ala Gln Gly Pro Pro Leu Gln
 1160 1165 1170
 Gly Gly Phe Asn Leu Gln Gly Gln Ser Pro Ser Phe Asn Ser Met Met Gly Gln
 1175 1180 1185 1190
 50 Ile Ser Gln Gln Gly Ser Phe Pro Leu Gln Gly Met His Pro Arg Ala Gly Leu
 1195 1200 1205
 Val Arg Pro Arg Thr Asn Thr Pro Lys Gln Leu Arg Met Gln Leu Gln Gln Arg
 1210 1215 1220 1225
 Leu Gln Gly Gln Gln Phe Leu Asn Gln Ser Arg Gln Ala Leu Glu Met Lys Met
 1230 1235 1240 1245
 55 Glu Asn Pro Ala Gly Thr Ala Val Met Arg Pro Met Met Pro Gln Ala Phe Phe
 1250 1255 1260
 Asn Ala Gln Met Ala Ala Gln Gln Lys Arg Glu Leu Met Ser His His Leu Gln
 1265 1270 1275 1280
 60 Gln Gln Arg Met Ala Met Met Met Ser Gln Pro Gln Pro Gln Ala Phe Ser Pro
 1285 1290 1295
 Pro Pro Asn Val Thr Ala Ser Pro Ser Met Asp Gly Val Leu Ala Gly Ser Ala
 1300 1305 1310 1315
 Met Pro Gln Ala Pro Pro Gln Gln Phe Pro Tyr Pro Ala Asn Tyr Gly Met Gly
 1320 1325 1330 1335
 65 Gln Pro Pro Glu Pro Ala Phe Gly Arg Gly Ser Ser Pro Pro Ser Ala Met Met
 1340 1345 1350
 Ser Ser Arg Met Gly Pro Ser Gln Asn Ala Met Val Gln His Pro Gln Pro Thr
 1355 1360 1365 1370
 70 Pro Met Tyr Gln Pro Ser Asp Met Lys Gly Trp Pro Ser Gly Asn Leu Ala Arg
 1375 1380 1385
 Asn Gly Ser Phe Pro Gln Gln Gln Phe Ala Pro Gln Gly Asn Pro Ala Ala Tyr

1390 1395 1400 1405
Asn Met Val His Met Asn Ser Ser Gly Gly His Leu Gly Gln Met Ala Met Thr
1410 1415 1420
5 Pro Met Pro Met Ser Gly Met Pro Met Gly Pro Asp Gln Lys Tyr Cys *** His
1425 1430 1435 1440
Leu Pro Ser Gly Thr Asp Cys Thr Asp Asp Thr Ala Gln Asp His Gln Asp Val
1445 1450 1455
Ala Ala Ser His Cys Leu Ser Ile Gln Leu Gly Asn Lys Ala Ser Val Thr Ser
1460 1465 1470 1475
10 Ser Gly Val Cys Ala Val Ile ***
1480 1485 1490 1495